

SEQUENCE LISTING

<110> Yano, Tetsuya; Nomoto, Tsuyoshi; Imamura, Takeshi; Canon Kabushiki Kaisha
<120> DNA Fragment Carrying Toluene Monooxygenase Gene, Recombinant Plasmid,
Transformed Microorganism, Method for Degrading Chlorinated Aliphatic Hydrocarbon
Compounds and Aromatic Compounds, and Method for Environmental Remediation
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gcgaaat ta acttcgcgtc agggcttcc ctgaattatc gagattttt gctgcctggg 180
tcgaacgtgg cacggatgct gcattgaagt ccggcatgga ggcgacacccg atc 233
atg aat cag cac ccc acc gat ctt tcc ccg ttc gat ccc ggc cgc aag 281
Met Asn Gln His Pro Thr Asp Leu Ser Pro Phe Asp Pro Gly Arg Lys
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Cys Val Arg Val Thr Gly Thr Asn Ala Arg Gly Phe Val Glu Phe Glu
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ctg tcg atc ggc ggc gcg ccg gaa ctg tgc gtc gag ctg acg ttg tct 377
Leu Ser Ile Gly Gly Ala Pro Glu Leu Cys Val Glu Leu Thr Leu Ser
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cct gcc gcc ttc gat gcg ttc tgc cgc gaa cag cag gtc acg cgg ctc 425
Pro Ala Ala Phe Asp Ala Phe Cys Arg Glu Gln Gln Val Thr Arg Leu
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gac gtc gaa gcg aac cca 443
Asp Val Glu Ala Asn Pro
65 70
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gtg acc atc gag ctg aag aca gtc gac atc aag ccg ctc cgg cac acc 510
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Phe Ala His Val Ala Gln Asn Ile Gly Gly Asp Lys Thr Ala Thr Arg
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Tyr Gln Glu Gly Met Met Gly Ala Gln Pro Gln Glu Asn Phe His Tyr
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Arg Pro Thr Trp Asp Pro Asp Tyr Glu Ile Phe Asp Pro Ser Arg Ser
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Tyr Tyr Ala Ser Trp Ala Thr Thr Arg Ala Arg Gln Gln Asp Ala Met

Part
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cg^c gac gac gtg gcc g^c cg^g g^c ctc gac gtg ctg gtg cc^g ctg cgc 846
Arg Asp Asp Val Ala Ala Arg Ala Leu Asp Val Leu Val Pro Leu Arg

115 120 125

ca^c gcc g^c tgg g^c g^c aac atg aac aac g^c g^c cag atc tgc g^c ctc 894
His Ala Ala Trp Gly Ala Asn Met Asn Asn Ala Gln Ile Cys Ala Leu

130 135 140

ggc tac ggc acg gtg ttc acc g^c ccc g^c g^c atg ttc cat g^c g^c atg gac 942
Gly Tyr Gly Thr Val Phe Thr Ala Pro Ala Met Phe His Ala Met Asp

145 150 155 160

aac ctc ggc gtc g^c caa tac ctc acg cgt ctc g^c ctc g^c atg g^c 990
Asn Leu Gly Val Ala Gln Tyr Leu Thr Arg Leu Ala Leu Ala Met Ala

165 170 175

gag ccc gac gtg ctg gag g^c g^c aag g^c acc tgg acc cgc gac g^c 1038
Glu Pro Asp Val Leu Glu Ala Ala Lys Ala Thr Trp Thr Arg Asp Ala

180 185 190

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Ala Trp Gln Pro Leu Arg Arg Tyr Val Glu Asp Thr Leu Val Val Ala

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ctg tat cc^g ctc gtc tac gac cgc ttc g^c g^c gac gaa cg^g atc g^c ctc 1182
Leu Tyr Pro Leu Val Tyr Asp Arg Phe Val Asp Glu Arg Ile Ala Leu

225 230 235 240

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Glu Gly Gly Ser Ala Val Ala Met Leu Thr Ala Phe Met Pro Glu Trp

245 250 255

cac acc gag tcg aac cgc tgg atc gac g^c g^c g^c gtg aag acg atg g^c 1278
His Thr Glu Ser Asn Arg Trp Ile Asp Ala Val Val Lys Thr Met Ala

260 265 270

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Ala Glu Ser Asp Asp Asn Arg Ala Leu Leu Ala Arg Trp Thr Arg Asp

275 280 285

See
Part
Cont.

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Trp Ser Ala Arg Ala Glu Ala Ala Leu Ala Pro Val Ala Ala Arg Ala
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Leu Gln Asp Ala Gly Arg Ala Ala Leu Asp Glu Val Arg Glu Gln Phe
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His Ala Arg Ala Ala Arg Leu Gly Ile Ala Leu
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Ser Pro Gly Met Val Lys Ile Asp Ala Pro Asp Arg Leu Thr Ile Arg
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Asp Glu Phe Thr Leu Ser Trp Ser His
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gcg gca atg acg cgc ggc ctc ggc tgg gag acg acc tac cag ccg atg 1898
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Asp Lys Val Phe Pro Tyr Asp Arg Tyr Glu Gly Ile Lys Ile His Asp

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aaa tac cag ggc gag aag gaa aag aag ctg tac gcg gtg atc gac gcg 2042
Lys Tyr Gln Gly Glu Lys Glu Lys Lys Leu Tyr Ala Val Ile Asp Ala
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Phe Thr Gln Asn Asn Ala Phe Leu Gly Val Ser Asp Ala Arg Tyr Ile
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Asn Ala Leu Lys Leu Phe Leu Gln Gly Val Thr Pro Leu Glu Tyr Leu
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Ala His Arg Gly Phe Ala His Val Gly Arg His Phe Thr Gly Glu Gly
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Gln Thr Glu Thr His Ala Met Ser Thr Tyr Asn Lys Phe Phe Asn Gly
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Phe His His Ser Asn Gln Trp Phe Asp Arg Val Trp Tyr Leu Ser Val
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Pro Lys Ser Phe Phe Glu Asp Ala Tyr Ser Ser Gly Pro Phe Glu Phe
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Leu Thr Ala Val Ser Phe Ser Phe Glu Tyr Val Leu Thr Asn Leu Leu
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Phe Val Pro Phe Met Ser Gly Ala Ala Tyr Asn Gly Asp Met Ser Thr
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Val Thr Phe Gly Phe Ser Ala Gln Ser Asp Glu Ser Arg His Met Thr
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245 250 255

gtg ccg atc gtg cag cgc tgg atc gac aag tgg ttc tgg cgc ggc tac 2618
Val Pro Ile Val Gln Arg Trp Ile Asp Lys Trp Phe Trp Arg Gly Tyr
260 265 270

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Arg Leu Leu Thr Leu Val Ala Met Met Met Asp Tyr Met Gln Pro Lys
275 280 285

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Arg Val Met Ser Trp Arg Glu Ser Trp Glu Met Tyr Ala Glu Gln Asn
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Lys Gly Trp Gln Asp Ala Cys Glu Gly Lys Asp His Ile Ser His Gln
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Cys Gln Thr Cys Gln Ile Pro Met Leu Phe Thr Glu Pro Gly Asn Pro
405 410 415

acg aag atc ggc gcg cgc gaa tgc aac tac ctc ggc aac aag ttc cac 3098
Thr Lys Ile Gly Ala Arg Glu Ser Asn Tyr Leu Gly Asn Lys Phe His
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atg agc cac caa ctt acc atc gag ccg ctg ggc gtc acg atc gag gtc 3857
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Met Asp Phe Glu Arg Glu Glu Gly Lys Ala Leu Ala Cys Cys Ala Thr
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115 120 125

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Pro Ile Arg Phe Gln Ala Gly Gln Tyr Val Gln Leu Glu Ile Pro Gly
130 135 140

ctc ggg cag agc cgc gcg ttc tcg atc gcg aac gcg ccg gcc gac gtc 4289
Leu Gly Gln Ser Arg Ala Phe Ser Ile Ala Asn Ala Pro Ala Asp Val
145 150 155 160

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180 185 190

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Arg Leu Ser Gly Pro Tyr Gly Arg Phe Phe Val Arg Arg Ser Ala Ala
195 200 205

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210 215 220

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Ser Met Ile ala asp Leu Leu ala Ser gly Val thr ala Pro Ile thr
225 230 235 240

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Leu Val tyr gly gln arg Ser ala gln glu Leu tyr tyr His asp glu
245 250 255

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Phe arg ala Leu ala glu arg His Pro asp Phe thr tyr Val Pro ala
260 265 270

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325 330 335

tcc atc tcc gct gcc gac gct caa cag acg cgc agc ccg ctg ttc cgg 4865
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Glu Arg Tyr Ala Cys Val Ser Gly Glu Ser Leu Leu Ala Gly Met Ala
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Lys Leu Gly Arg Arg Gly Ile Pro Val Gly Cys Leu Asn Gly Gly Cys
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Pro Ile Ser Arg Ala His Val Ser Ala Glu Glu Glu Asn Asp Gly Tyr
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Ala Leu Ala Cys Arg Val Val Pro Asp Gly Asp Val Glu Leu Glu Val
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gcc ggc cgg ctc agg aag ccg ttc ttc tgc ggc atg gca tgt gcc ggc 5211
Ala Gly Arg Leu Arg Lys Pro Phe Phe Cys Gly Met Ala Cys Ala Gly
100 105 110
acg gcg gcg atc aac aag 5229
Thr Ala Ala Ile Asn Lys
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Met Glu Ala Thr Pro Ile Met Asn Gln His Pro Thr Asp Leu Ser Pro

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Phe Asp Pro Gly Arg Lys Cys Val Arg Val Thr Gly Thr Asn Ala Arg

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Gly Phe Val Glu Phe Glu Leu Ser Ile Gly Gly Ala Pro Glu Leu Cys

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Val Glu Leu Thr Leu Ser Pro Ala Ala Phe Asp Ala Phe Cys Arg Glu

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Gln Gln Val Thr Arg Leu Asp Val Glu Ala Asn Pro

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<213> Burkholderia cepacia

<220>

<223> TomL polypeptide

<400> 3

Met Arg Ser Ala Ala Asn Ser Arg Ser Arg Gly Ser Thr Ser Lys Arg

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Thr His Asp Leu Glu Glu Gln Glu Val Thr Ile Glu Leu Lys Thr Val

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Asp Ile Lys Pro Leu Arg His Thr Phe Ala His Val Ala Gln Asn Ile

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Gly Gly Asp Lys Thr Ala Thr Arg Tyr Gln Glu Gly Met Met Gly Ala

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Gln Pro Gln Glu Asn Phe His Tyr Arg Pro Thr Trp Asp Pro Asp Tyr

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Glu Ile Phe Asp Pro Ser Arg Ser Ala Ile Arg Met Ala Asn Trp Tyr

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Ala Leu Lys Asp Pro Arg Gln Phe Tyr Tyr Ala Ser Trp Ala Thr Thr

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*Subj of
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Arg Ala Arg Gln Gln Asp Ala Met Glu Ser Asn Phe Glu Phe Val Glu
115 120 125
Ser Arg Arg Met Ile Gly Leu Met Arg Asp Asp Val Ala Ala Arg Ala
130 135 140
Leu Asp Val Leu Val Pro Leu Arg His Ala Ala Trp Gly Ala Asn Met
145 150 155 160
Asn Asn Ala Gln Ile Cys Ala Leu Gly Tyr Gly Thr Val Phe Thr Ala
165 170 175
Pro Ala Met Phe His Ala Met Asp Asn Leu Gly Val Ala Gln Tyr Leu
180 185 190
Thr Arg Leu Ala Leu Ala Met Ala Glu Pro Asp Val Leu Glu Ala Ala
195 200 205
Lys Ala Thr Trp Thr Arg Asp Ala Ala Trp Gln Pro Leu Arg Arg Tyr
210 215 220
Val Glu Asp Thr Leu Val Val Ala Asp Pro Val Glu Leu Phe Ile Ala
225 230 235 240
Gln Asn Leu Ala Leu Asp Gly Leu Leu Tyr Pro Leu Val Tyr Asp Arg
245 250 255
Phe Val Asp Glu Arg Ile Ala Leu Glu Gly Ser Ala Val Ala Met
260 265 270
Leu Thr Ala Phe Met Pro Glu Trp His Thr Glu Ser Asn Arg Trp Ile
275 280 285
Asp Ala Val Val Lys Thr Met Ala Ala Glu Ser Asp Asp Asn Arg Ala
290 295 300
Leu Leu Ala Arg Trp Thr Arg Asp Trp Ser Ala Arg Ala Glu Ala Ala
305 310 315 320
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20 25 30
Ser Pro Gly Met Val Lys Ile Asp Ala Pro Asp Arg Leu Thr Ile Arg
35 40 45
Arg Glu Thr Ile Glu Glu Leu Thr Gly Thr Arg Phe Asp Leu Gln Gln
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65 70 75 80
Asp Glu Phe Thr Leu Ser Trp Ser His
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<223> TomN polypeptide

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Ala Ala Met Thr Arg Gly Leu Gly Trp Glu Thr Thr Tyr Gln Pro Met
20 25 30
Asp Lys Val Phe Pro Tyr Asp Arg Tyr Glu Gly Ile Lys Ile His Asp
35 40 45
Trp Asp Lys Trp Val Asp Pro Phe Arg Leu Thr Met Asp Ala Tyr Trp
50 55 60
Lys Tyr Gln Gly Glu Lys Glu Lys Lys Leu Tyr Ala Val Ile Asp Ala
65 70 75 80
Phe Thr Gln Asn Asn Ala Phe Leu Gly Val Ser Asp Ala Arg Tyr Ile
85 90 95
Asn Ala Leu Lys Leu Phe Leu Gln Gly Val Thr Pro Leu Glu Tyr Leu
100 105 110
Ala His Arg Gly Phe Ala His Val Gly Arg His Phe Thr Gly Glu Gly
115 120 125
Ala Arg Ile Ala Cys Gln Met Gln Ser Ile Asp Glu Leu Arg His Tyr

Sub A
cont

130 135 140
Gln Thr Glu Thr His Ala Met Ser Thr Tyr Asn Lys Phe Phe Asn Gly
145 150 155 160
Phe His His Ser Asn Gln Trp Phe Asp Arg Val Trp Tyr Leu Ser Val
165 170 175
Pro Lys Ser Phe Phe Glu Asp Ala Tyr Ser Ser Gly Pro Phe Glu Phe
180 185 190
Leu Thr Ala Val Ser Phe Ser Phe Glu Tyr Val Leu Thr Asn Leu Leu
195 200 205
Phe Val Pro Phe Met Ser Gly Ala Ala Tyr Asn Gly Asp Met Ser Thr
210 215 220
Val Thr Phe Gly Phe Ser Ala Gln Ser Asp Glu Ser Arg His Met Thr
225 230 235 240
Leu Gly Ile Glu Cys Ile Lys Phe Leu Leu Glu Gln Asp Pro Asp Asn
245 250 255
Val Pro Ile Val Gln Arg Trp Ile Asp Lys Trp Phe Trp Arg Gly Tyr
260 265 270
Arg Leu Leu Thr Leu Val Ala Met Met Met Asp Tyr Met Gln Pro Lys
275 280 285
Arg Val Met Ser Trp Arg Glu Ser Trp Glu Met Tyr Ala Glu Gln Asn
290 295 300
Gly Gly Ala Leu Phe Lys Asp Leu Ala Arg Tyr Gly Ile Arg Glu Pro
305 310 315 320
Lys Gly Trp Gln Asp Ala Cys Glu Gly Lys Asp His Ile Ser His Gln
325 330 335
Ala Trp Ser Thr Phe Tyr Gly Phe Asn Ala Ala Ser Ala Phe His Thr
340 345 350
Trp Val Pro Thr Glu Asp Glu Met Gly Trp Leu Ser Ala Lys Tyr Pro
355 360 365
Asp Ser Phe Asp Arg Tyr Tyr Arg Pro Arg Phe Asp His Trp Gly Glu
370 375 380
Gln Ala Arg Ala Gly Asn Arg Phe Tyr Met Lys Thr Leu Pro Met Leu
385 390 395 400
Cys Gln Thr Cys Gln Ile Pro Met Leu Phe Thr Glu Pro Gly Asn Pro
405 410 415
Thr Lys Ile Gly Ala Arg Glu Ser Asn Tyr Leu Gly Asn Lys Phe His
420 425 430

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Phe Cys Ser Asp His Cys Lys Asp Ile Phe Asp His Glu Pro Gln Lys
435 440 445

Tyr Val Gln Ala Trp Leu Pro Val His Gln Ile His Gln Gly Asn Cys
450 455 460

Phe Pro Pro Asp Ala Asp Pro Gly Ala Glu Gly Phe Asp Pro Leu Ala
465 470 475 480

Ala Val Leu Asp Tyr Tyr Ala Val Thr Met Gly Arg Asp Asn Leu Asp
485 490 495

Phe Asp Gly Ser Glu Asp Gln Lys Asn Phe Ala Ala Trp Arg Gly Gln
500 505 510

Ala Thr Arg Asn
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<223> TomO polypeptide

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5 10 15

Val Glu Lys Phe Pro Ala Pro Leu Leu Tyr Val Cys Trp Glu Asn His
20 25 30

Leu Met Phe Pro Ala Pro Phe Cys Leu Pro Leu Pro Pro Asp Met Pro
35 40 45

Phe Gly Ala Leu Ala Gly Asp Val Leu Pro Pro Val Tyr Gly Tyr His
50 55 60

Pro Asp Phe Ala Lys Ile Asp Trp Asp Arg Val Glu Trp Phe Arg Ser
65 70 75 80

Gly Glu Pro Trp Ala Pro Asp Pro Ala Lys Ser Leu Ala Gly Asn Gly
85 90 95

Leu Gly His Lys Asp Leu Ile Ser Phe Arg Thr Pro Gly Leu Asp Gly
100 105 110

Leu Gly Gly Ala Ser Phe
115

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*Part A
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Phe Arg Ala Leu Ala Glu Arg His Pro Asn Phe Thr Tyr Val Pro Ala
260 265 270

Leu Ser Glu Gly Ala Pro His Ala Gly Gly Asp Val Ala Gln Gly Phe
275 280 285

Val His Asp Val Ala Lys Ala His Phe Gly Gly Asp Phe Ser Gly His
290 295 300

Gln Ala Tyr Leu Cys Gly Pro Pro Ala Met Ile Asp Ala Cys Ile Thr
305 310 315 320

Thr Leu Met Gln Gly Arg Leu Phe Glu Arg Asp Ile Tyr His Glu Lys
325 330 335

Phe Ile Ser Ala Ala Asp Ala Gln Gln Thr Arg Ser Pro Leu Phe Arg
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<210> 8

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<213> *Burkholderia cepacia*

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Glu Arg Tyr Ala Cys Val Ser Gly Glu Ser Leu Leu Ala Gly Met Ala
20 25 30

Lys Leu Gly Arg Arg Gly Ile Pro Val Gly Cys Leu Asn Gly Gly Cys
35 40 45

Gly Val Cys Lys Val Arg Val Leu Arg Gly Ala Val Arg Lys Leu Gly
50 55 60

Pro Ile Ser Arg Ala His Val Ser Ala Glu Glu Glu Asn Asp Gly Tyr
65 70 75 80

Ala Leu Ala Cys Arg Val Val Pro Asp Gly Asp Val Glu Leu Glu Val
85 90 95

Ala Gly Arg Leu Arg Lys Pro Phe Phe Cys Gly Met Ala Cys Ala Gly
100 105 110

Thr Ala Ala Ile Asn Lys
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Sub Al Cont.